



September 19, 2002

APPLICATION SERIAL NUMBER

09902481

**DOES NOT COMPLY WITH THE
SEQUENCE RULES. See reasons below.**

**CRF, paper copy of sequence listing and
statement that both are same missing.**

**The sequences disclosed on page 29, lines 1-
7, of the specification need to be in CRF
and paper copy of the sequence listing, but
are missing.**

Kevin



#14

SEQUENCE LISTING

<110> Springer, Timothy
Shimaoka, Motomu
Shifman, Julia
Mayo, Stephen

<120> NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY

<130> A-70586-1/RFT/RMS/RMK

<140> US 09/902,481

<141> 2001-07-09

<150> US 60/216,600

<151> 2000-07-07

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 1153

<212> PRT

<213> Homo sapiens

<220>

<221> mat_peptide

<222> (17)..()

<223>

<400> 1

Met Ala Leu Arg Val Leu Leu Leu Thr Ala Leu Thr Leu Cys His Gly
-15 -10 -5 -1

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
180 185 190

Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
195 200 205

Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu

305		310		315		320
Gly Thr Gln Thr	Gly Ser Ser Ser Ser	Phe Glu His Glu Met Ser Gln				
	325	330			335	
Glu Gly Phe Ser	Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr					
	340	345			350	
Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys						
	355	360			365	
Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn						
	370	375			380	
Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val						
	385	390			395	400
Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val						
	405			410		415
Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val						
	420		425			430
Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val						
	435		440			445
Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro						
	450		455			460
His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu						
	465		470			475
Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly						
	485			490		495
Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu						
	500			505		510
Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro						
	515		520			525
Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser						
	530		535			540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
 545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
 565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
 580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
 595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
 610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
 625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
 645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
 660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
 675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
 690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
 705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
 725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
 740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
 755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
 770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
 785 790 795 800

Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
 805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
 820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
 835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
 850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
 865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
 885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
 900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
 915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
 930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
 945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
 965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
 980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
 995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
 1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
 1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
 1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
 1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
 1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
 1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
 1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu
 1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln
 1130 1135

<210> 2
 <211> 4740
 <212> DNA
 <213> Homo sapiens

<400> 2
 gaattccgtg gttcctcagt ggtgcctgca acccctgggt cacctccttc caggttctgg 60
 ctcttccag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg 120
 ttcaacttgg aactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag 180
 agcgtggtcc agcttcaggg atccaggggtg gtggttgag cccccagga gatagtggct 240
 gccaacaaa ggggcagcct ctaccagtgc gactacagca caggctcatg cgagcccatc 300
 cgctgcagg tccccgtgga ggccgtgaac atgtccctgg gcctgtcctt ggcagccacc 360

accagcccc	ctcagctgct	ggcctgtggt	cccaccgtgc	accagacttg	cagtgagaac	420
acgtatgtga	aagggctctg	cttcctgttt	ggatccaacc	tacggcagca	gccccagaag	480
ttcccagagg	ccctccgagg	gtgtcctcaa	gaggatagtg	acattgcctt	cttgattgat	540
ggctctggta	gcatcatccc	acatgacttt	cggcggatga	aggagtttgt	ctcaactgtg	600
atggagcaat	taaaaaagtc	caaaaccttg	ttctctttga	tgcagtactc	tgaagaattc	660
cggattcact	ttaccttcaa	agagttccag	aacaacccta	acccaagatc	actggtgaag	720
ccaataacgc	agctgcttgg	gcggacacac	acggccacgg	gcatccgcaa	agtggtagca	780
gagctgttta	acatcaccaa	cggagcccga	aagaatgcct	ttaagatcct	agttgtcatc	840
acggatggag	aaaagtttgg	cgatcccttg	ggatatgagg	atgtcatccc	tgaggcagac	900
agagagggag	tcattcgcta	cgtcattggg	gtgggagatg	ccttccgcag	tgagaaatcc	960
cgccaagagc	ttaataccat	cgcacccaag	ccgcctcgtg	atcacgtgtt	ccaggtgaat	1020
aactttgagg	ctctgaagac	cattcagaac	cagcttcggg	agaagatctt	tgcgatcgag	1080
ggtactcaga	caggaagtag	cagctccttt	gagcatgaga	tgtctcagga	aggcttcagc	1140
gctgccatca	cctctaattg	ccccttgctg	agcactgtgg	ggagctatga	ctgggctggt	1200
ggagtctttc	tatatacatc	aaaggagaaa	agcaccttca	tcaacatgac	cagagtggat	1260
tcagacatga	atgatgctta	cttgggttat	gctgccgcca	tcattcttacg	gaaccgggtg	1320
caaagcctgg	ttctgggggc	acctcgatat	cagcacatcg	gcctggtagc	gatgttcagg	1380
cagaacactg	gcatgtggga	gtccaacgct	aatgtcaagg	gcaccagat	cggcgcctac	1440
ttcggggcct	ccctctgctc	cgtggacgtg	gacagcaacg	gcagcaccga	cctggtcctc	1500
atcggggccc	cccattacta	cgagcagacc	cgagggggcc	aggtgtccgt	gtgccccttg	1560
cccagggggc	agagggctcg	gtggcagtgt	gatgctgttc	tctacgggga	gcagggccaa	1620
ccctggggcc	gctttggggc	agccctaaca	gtgctggggg	acgtaaatgg	ggacaagctg	1680
acggacgtgg	ccattggggc	cccaggagag	gaggacaacc	ggggtgctgt	ttacctgttt	1740
cacggaacct	caggatctgg	catcagcccc	tcccatagcc	agcggatagc	aggctccaag	1800
ctctctccca	ggctccagta	ttttggtcag	tactgagtg	ggggccagga	cctcacaatg	1860
gatggactgg	tagacctgac	tgtaggagcc	caggggcacg	tgctgctgct	caggtcccag	1920
ccagtactga	gagtcaaggc	aatcatggag	ttcaatccca	gggaagtggc	aaggaatgta	1980
tttgagtgtg	atgatcaggt	ggtgaaaggc	aaggaagccg	gagaggtcag	agtctgcctc	2040

catgtccaga	agagcacacg	ggatcggcta	agagaaggac	agatccagag	tgttgtgact	2100
tatgacctgg	ctctggactc	cggccgcca	cattcccgcg	ccgtcttcaa	tgagacaaag	2160
aacagcacac	gcagacagac	acaggtcttg	gggctgaccc	agacttgatga	gaccctgaaa	2220
ctacagttgc	cgaattgcat	cgaggaccca	gtgagcccca	ttgtgctgcg	cctgaacttc	2280
tctctggtgg	gaacgccatt	gtctgctttc	gggaacctcc	ggccagtgc	ggcggaggat	2340
gctcagagac	tcttcacagc	cttggtttccc	tttgagaaga	attgtggcaa	tgacaacatc	2400
tgccaggatg	acctcagcat	caccttcagt	ttcatgagcc	tggactgcct	cgtggtgggt	2460
gggccccggg	agttcaacgt	gacagtgcct	gtgagaaatg	atggtgagga	ctcctacagg	2520
acacaggtca	ccttcttctt	cccgtttgac	ctgtcctacc	ggaaggtgtc	cacactccag	2580
aaccagcgct	cacagcgatc	ctggcgcttg	gcctgtgagt	ctgcctcttc	caccgaagtg	2640
tctggggcct	tgaagagcac	cagctgcagc	ataaaccacc	ccatcttccc	ggaaaactca	2700
gaggtcacct	ttaatatcac	gtttgatgta	gactctaagg	cttcccttgg	aaacaaactg	2760
ctcctcaagg	ccaatgtgac	cagtgcagac	aacatgccca	gaaccaacaa	aaccgaattc	2820
caactggagc	tgccggtgaa	atatgctgtc	tacatggtgg	tcaccagcca	tggggtctcc	2880
actaaatatc	tcaacttcac	ggcctcagag	aataccagtc	gggtcatgca	gcacaaatat	2940
caggtcagca	acctggggca	gaggagcctc	cccatcagcc	tggtgttctt	ggtgcccgtc	3000
cggctgaacc	agactgtcat	atgggaccgc	ccccaggcca	ccttctccga	gaacctctcg	3060
agtacgtgcc	acaccaagga	gcgcttgccc	tctcactccg	actttctggc	tgagcttcgg	3120
aaggccccc	tggtgaactg	ctccatcgct	gtctgccaga	gaatccagtg	tgacatcccc	3180
ttcttttgga	tccaggaaga	attcaatgct	accctcaaag	gcaacctctc	gtttgactgg	3240
tacatcaaga	cctcgcataa	ccacctctcg	atcgtgagca	cagctgagat	cttgtttaac	3300
gattccgtgt	tcacctgct	gccgggacag	ggggcgcttg	tgaggcccca	gacggagacc	3360
aaagtggagc	cgttcgaggt	ccccaacccc	ctgccgtcca	tcgtgggcag	ctctgtcggg	3420
ggactgctgc	tcctggccct	catcaccgcc	gcgctgtaca	agctcggctt	cttcaagcgg	3480
caatacaagg	acatgatgag	tgaagggggg	ccccggggg	ccgaaccca	gtagcggctc	3540
cttcccga	gagctgcctc	tcggtggcca	gcaggactct	gccagacca	cacgtagccc	3600
ccaggctgct	ggacacgtcg	gacagcgaag	tatccccgac	aggacgggct	tggtgttcca	3660
tttgtgtgtg	tgcaagtgtg	tatgtgcgtg	tgtgcgagtg	tgtgcaagtg	tctgtgtgca	3720
agtgtgtgca	cgtgtgcgtg	tgctgtcatg	tgactcgcga	cgcccatgtg	tgagtgtgtg	3780

caagtatgtg agtgtgtcca gtgtgtgtgc gtgtgtccat gtgtgtgcag tgtgtgcatg 3840
 tgtgagtgagtg tgtgcatgtg tgtgctcagg ggctgtggct cacgtgtgtg actcagagtg 3900
 tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggcagaaggg aactgcctgg 3960
 gctcccttgt gcgtgggtaa gccgctgctg ggttttcctc cgggagaggg gacgggtcaat 4020
 cctgtgggtg aagagagagg gaaacacagc agcatctctc cactgaaaga agtgggactt 4080
 cccgtcgcct gcgagcctgc ggctgtgctg agcctgcgca gcttggatgg atactccatg 4140
 agaaaagccg tgggtggaac caggagcctc ctccacacca gcgctgatgc ccaataaaga 4200
 tgcccactga ggaatcatga agcttccttt ctggattcat ttattatttc aatgtgactt 4260
 taattttttg gatggataag cctgtctatg gtacaaaaat cacaaggcat tcaagtgtac 4320
 agtgaaaagt ctccctttcc agatattcaa gtcacctcct taaaggtagt caagattgtg 4380
 ttttgagggt tccttcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac 4440
 accacacaca tacacacaca caagcttttt tacacaaatg gtagcatact ttatattggg 4500
 ctgtatcttg ctttttttca ccaatatttc tcagacatcg gttcatatta agacataaat 4560
 tactttttca ttcttttata ccgctgcata gtattccatt gtgtgagtgt accataatgt 4620
 atttaaccag tcttcttttg atatactatt ttcattctctt gttattgcat ctgctgagtt 4680
 aataaatcaa atatatgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4740

<210> 3
 <211> 1137
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic

<400> 3

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
 1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val

50	55	60
Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr 65 70 75 80		
Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr 85 90 95		
Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser 100 105 110		
Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys 115 120 125		
Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser 130 135 140		
Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Leu Val Ser Thr Ile 145 150 155 160		
Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr 165 170 175		
Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn 180 185 190		
Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg 195 200 205		
Thr His Thr Ala Thr Gly Leu Arg Lys Val Val Arg Glu Leu Phe Asn 210 215 220		
Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Phe Leu Leu 225 230 235 240		
Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile 245 250 255		
Pro Glu Leu Asp Arg Glu Gly Val Ile Arg Tyr Val Leu Gly Phe Gly 260 265 270		
Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Val Ala 275 280 285		

Ser Lys Pro Pro Arg Asp His Val Phe Gln Ala Asn Asn Phe Glu Ala
 290 295 300

Leu Lys Thr Val Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
 305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
 325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
 340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
 355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
 370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
 385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val
 405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val
 420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
 435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
 450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
 465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
 485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
 500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
 740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
 755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
 770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
 785 790 795 800

Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
 805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
 820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
 835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
 850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
 865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
 885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
 900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
 915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
 930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
 945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser

965

970

975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
 980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
 995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
 1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
 1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
 1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
 1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
 1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
 1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
 1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu
 1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln
 1130 1135

<210> 4
 <211> 1137
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic

<400> 4

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
 1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
 50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
 65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
 85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
 100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
 115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
 130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Trp Val Ser Thr Val
 145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
 165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
 180 185 190

Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg
 195 200 205

Thr His Thr Ala Thr Gly Leu Arg Lys Val Val Arg Glu Leu Phe Asn
 210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Phe Leu Leu

225		230		235		240									
Thr	Asp	Gly	Glu	Lys	Phe	Gly	Asp	Pro	Leu	Gly	Tyr	Glu	Asp	Val	Ile
				245					250					255	
Pro	Glu	Leu	Asp	Arg	Glu	Gly	Val	Ile	Arg	Tyr	Val	Ile	Gly	Val	Gly
			260					265					270		
Asp	Ala	Phe	Arg	Ser	Glu	Lys	Ser	Arg	Gln	Glu	Leu	Asn	Thr	Val	Ala
		275						280				285			
Ser	Lys	Pro	Pro	Arg	Asp	His	Val	Phe	Gln	Ile	Asn	Asn	Phe	Glu	Ala
	290					295					300				
Leu	Lys	Thr	Ile	Gln	Asn	Gln	Leu	Arg	Glu	Lys	Ile	Phe	Ala	Ile	Glu
305					310					315					320
Gly	Thr	Gln	Thr	Gly	Ser	Ser	Ser	Ser	Phe	Glu	His	Glu	Met	Ser	Gln
				325					330					335	
Glu	Gly	Phe	Ser	Ala	Ala	Ile	Thr	Ser	Asn	Gly	Pro	Leu	Leu	Ser	Thr
			340					345					350		
Val	Gly	Ser	Tyr	Asp	Trp	Ala	Gly	Gly	Val	Phe	Leu	Tyr	Thr	Ser	Lys
		355					360					365			
Glu	Lys	Ser	Thr	Phe	Ile	Asn	Met	Thr	Arg	Val	Asp	Ser	Asp	Met	Asn
	370					375					380				
Asp	Ala	Tyr	Leu	Gly	Tyr	Ala	Ala	Ala	Ile	Ile	Leu	Arg	Asn	Arg	Val
385					390				395						400
Gln	Ser	Leu	Val	Leu	Gly	Ala	Pro	Arg	Tyr	Gln	His	Ile	Gly	Leu	Val
				405					410					415	
Ala	Met	Phe	Arg	Gln	Asn	Thr	Gly	Met	Trp	Glu	Ser	Asn	Ala	Asn	Val
			420					425					430		
Lys	Gly	Thr	Gln	Ile	Gly	Ala	Tyr	Phe	Gly	Ala	Ser	Leu	Cys	Ser	Val
		435					440					445			
Asp	Val	Asp	Ser	Asn	Gly	Ser	Thr	Asp	Leu	Val	Leu	Ile	Gly	Ala	Pro
	450					455					460				

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
 465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
 485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
 500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
 515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
 530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
 545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
 565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
 580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
 595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
 610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
 625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
 645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
 660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
 675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
785 790 795 800

Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
 915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
 930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
 945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
 965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
 980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
 995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
 1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
 1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
 1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
 1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
 1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
 1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
 1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu
 1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln

1130

1135

<210> 5
 <211> 1137
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic

<400> 5

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
 1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
 50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
 65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
 85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
 100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
 115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Val Asp Gly Ser Gly Ser
 130 135 140

Ile Ile Pro His Asp Phe Arg Arg Ala Lys Glu Phe Ile Ser Thr Val
 145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
 165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
180 185 190

Pro Asn Pro Arg Ser Leu Ile Lys Pro Ile Thr Gln Leu Leu Gly Arg
195 200 205

Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Ile Leu Ile
225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Val Ala
275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Ile Asn Asn Phe Glu Ala
290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val

405					410					415					
Ala	Met	Phe	Arg	Gln	Asn	Thr	Gly	Met	Trp	Glu	Ser	Asn	Ala	Asn	Val
			420					425					430		
Lys	Gly	Thr	Gln	Ile	Gly	Ala	Tyr	Phe	Gly	Ala	Ser	Leu	Cys	Ser	Val
		435					440					445			
Asp	Val	Asp	Ser	Asn	Gly	Ser	Thr	Asp	Leu	Val	Leu	Ile	Gly	Ala	Pro
	450					455					460				
His	Tyr	Tyr	Glu	Gln	Thr	Arg	Gly	Gly	Gln	Val	Ser	Val	Cys	Pro	Leu
465					470					475					480
Pro	Arg	Gly	Gln	Arg	Ala	Arg	Trp	Gln	Cys	Asp	Ala	Val	Leu	Tyr	Gly
				485					490					495	
Glu	Gln	Gly	Gln	Pro	Trp	Gly	Arg	Phe	Gly	Ala	Ala	Leu	Thr	Val	Leu
			500					505					510		
Gly	Asp	Val	Asn	Gly	Asp	Lys	Leu	Thr	Asp	Val	Ala	Ile	Gly	Ala	Pro
		515					520					525			
Gly	Glu	Glu	Asp	Asn	Arg	Gly	Ala	Val	Tyr	Leu	Phe	His	Gly	Thr	Ser
	530					535					540				
Gly	Ser	Gly	Ile	Ser	Pro	Ser	His	Ser	Gln	Arg	Ile	Ala	Gly	Ser	Lys
545						550					555				560
Leu	Ser	Pro	Arg	Leu	Gln	Tyr	Phe	Gly	Gln	Ser	Leu	Ser	Gly	Gly	Gln
				565					570					575	
Asp	Leu	Thr	Met	Asp	Gly	Leu	Val	Asp	Leu	Thr	Val	Gly	Ala	Gln	Gly
			580					585					590		
His	Val	Leu	Leu	Leu	Arg	Ser	Gln	Pro	Val	Leu	Arg	Val	Lys	Ala	Ile
		595					600					605			
Met	Glu	Phe	Asn	Pro	Arg	Glu	Val	Ala	Arg	Asn	Val	Phe	Glu	Cys	Asn
	610					615					620				
Asp	Gln	Val	Val	Lys	Gly	Lys	Glu	Ala	Gly	Glu	Val	Arg	Val	Cys	Leu
625					630					635					640

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly
580 585 590

His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile
595 600 605

Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn
610 615 620

Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu
625 630 635 640

His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
645 650 655

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
660 665 670

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
675 680 685

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
690 695 700

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
705 710 715 720

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
725 730 735

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
740 745 750

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
755 760 765

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
770 775 780

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
785 790 795 800

Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
805 810 815

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
 865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
 885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
 900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
 915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
 930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
 945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
 965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
 980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
 995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
 1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
 1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
 1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
 1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
 1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
 1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
 1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu
 1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln
 1130 1135

<210> 6
 <211> 1137
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic

<400> 6

Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
 1 5 10 15

Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
 20 25 30

Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
 35 40 45

Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
 50 55 60

Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
 65 70 75 80

Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
 85 90 95

Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
 100 105 110

Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
 115 120 125

Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
 130 135 140

Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
 145 150 155 160

Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
 165 170 175

Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
 180 185 190

Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
 195 200 205

Thr His Thr Ala Thr Gly Val Arg Lys Val Ile Arg Glu Leu Leu Asn
 210 215 220

Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Ile Val Ile
 225 230 235 240

Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
 245 250 255

Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
 260 265 270

Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
 275 280 285

Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
 290 295 300

Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
 305 310 315 320

Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
 325 330 335

Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
 340 345 350

Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
 355 360 365

Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
 370 375 380

Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
 385 390 395 400

Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val
 405 410 415

Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val
 420 425 430

Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
 435 440 445

Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
 450 455 460

His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
 465 470 475 480

Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly
 485 490 495

Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
 500 505 510

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro
 515 520 525

Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser
 530 535 540

Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys
 545 550 555 560

Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln
 565 570 575

Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly

580					585					590					
His	Val	Leu	Leu	Leu	Arg	Ser	Gln	Pro	Val	Leu	Arg	Val	Lys	Ala	Ile
		595					600					605			
Met	Glu	Phe	Asn	Pro	Arg	Glu	Val	Ala	Arg	Asn	Val	Phe	Glu	Cys	Asn
	610					615					620				
Asp	Gln	Val	Val	Lys	Gly	Lys	Glu	Ala	Gly	Glu	Val	Arg	Val	Cys	Leu
625					630					635					640
His	Val	Gln	Lys	Ser	Thr	Arg	Asp	Arg	Leu	Arg	Glu	Gly	Gln	Ile	Gln
				645					650					655	
Ser	Val	Val	Thr	Tyr	Asp	Leu	Ala	Leu	Asp	Ser	Gly	Arg	Pro	His	Ser
			660					665					670		
Arg	Ala	Val	Phe	Asn	Glu	Thr	Lys	Asn	Ser	Thr	Arg	Arg	Gln	Thr	Gln
		675					680					685			
Val	Leu	Gly	Leu	Thr	Gln	Thr	Cys	Glu	Thr	Leu	Lys	Leu	Gln	Leu	Pro
	690					695					700				
Asn	Cys	Ile	Glu	Asp	Pro	Val	Ser	Pro	Ile	Val	Leu	Arg	Leu	Asn	Phe
705					710					715					720
Ser	Leu	Val	Gly	Thr	Pro	Leu	Ser	Ala	Phe	Gly	Asn	Leu	Arg	Pro	Val
				725					730					735	
Leu	Ala	Glu	Asp	Ala	Gln	Arg	Leu	Phe	Thr	Ala	Leu	Phe	Pro	Phe	Glu
			740					745					750		
Lys	Asn	Cys	Gly	Asn	Asp	Asn	Ile	Cys	Gln	Asp	Asp	Leu	Ser	Ile	Thr
		755					760					765			
Phe	Ser	Phe	Met	Ser	Leu	Asp	Cys	Leu	Val	Val	Gly	Gly	Pro	Arg	Glu
	770					775					780				
Phe	Asn	Val	Thr	Val	Thr	Val	Arg	Asn	Asp	Gly	Glu	Asp	Ser	Tyr	Arg
785					790					795					800
Thr	Gln	Val	Thr	Phe	Phe	Phe	Pro	Leu	Asp	Leu	Ser	Tyr	Arg	Lys	Val
				805					810					815	

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
820 825 830

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
835 840 845

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
850 855 860

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
865 870 875 880

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
885 890 895

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
900 905 910

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
915 920 925

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
930 935 940

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
945 950 955 960

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
965 970 975

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
980 985 990

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
995 1000 1005

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly
1010 1015 1020

Ile Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe
1025 1030 1035

Asp Trp Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser
 1040 1045 1050

Thr Ala Glu Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro
 1055 1060 1065

Gly Gln Gly Ala Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu
 1070 1075 1080

Pro Phe Glu Val Pro Asn Pro Leu Pro Leu Ile Val Gly Ser Ser
 1085 1090 1095

Val Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Ala Leu Tyr
 1100 1105 1110

Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Asp Met Met Ser Glu
 1115 1120 1125

Gly Gly Pro Pro Gly Ala Glu Pro Gln
 1130 1135

<210> 7
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> stability sequence

<220>
 <221> MISC_FEATURE
 <222> (3)..(6)
 <223> "Xaa" at positions 3 through 6 can be any amino acid.

<400> 7

Met Gly Xaa Xaa Xaa Xaa Gly Gly Pro Pro
 1 5 10

<210> 8
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> example

<400> 8

Leu Val Leu Val Leu Val Leu
1 5

<210> 9

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 9

Leu Pro Leu Pro Leu Val Leu
1 5

<210> 10

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 10

Leu Pro Leu Pro Leu Pro Leu
1 5

<210> 11

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 11

Leu Pro Pro Pro Leu Val Leu
1 5

<210> 12

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> example

<400> 12

Leu Pro Pro Val Leu Pro Pro
1 5

<210> 13
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> example

<400> 13

Pro Pro Leu Pro Pro Val Pro
1 5